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Figure 1 Nucleotide sequence alignment of LGR6.1 and LGR6.2 and LGR6.

LGR6.1	(1)	1	80
LGR6.2	(1)		
LGR6	(1)		
LGR6.1	(81)	81	160
LGR6.2	(81)		
LGR6	(63)		
LGR6.1	(161)	161	240
LGR6.2	(161)		
LGR6	(142)		
LGR6.1	(241)	241	320
LGR6.2	(241)		
LGR6	(222)		
LGR6.1	(321)	321	400
LGR6.2	(321)		
LGR6	(300)		
LGR6.1	(401)	401	480
LGR6.2	(401)		
LGR6	(300)		
LGR6.1	(481)	481	560
LGR6.2	(481)		
LGR6	(300)		
LGR6.1	(561)	561	640
LGR6.2	(561)		
LGR6	(300)		
LGR6.1	(641)	641	720
LGR6.2	(641)		
LGR6	(334)		
LGR6.1	(721)	721	800
LGR6.2	(721)		
LGR6	(414)		
LGR6.1	(801)	801	880
LGR6.2	(801)		
LGR6	(494)		
LGR6.1	(881)	881	960
LGR6.2	(881)		
LGR6	(574)		
LGR6.1	(961)	961	1040
LGR6.2	(961)		
LGR6	(654)		
LGR6.1	(1027)	1041	1120
LGR6.2	(1041)		
LGR6	(720)		

Figure 1 (cont.)

		1121	1200
LGR6.1	(1027)	-----	-----
LGR6.2	(1121)	CTGCCCTAG	-----
LGR6	(720)	-----	-----
		1201	1280
LGR6.1	(1098)	-----	-----
LGR6.2	(1201)	-----	-----
LGR6	(791)	-----	-----
		1281	1360
6.1	(1178)	-----	-----
6.2	(1281)	-----	-----
GR6	(871)	-----	-----
		1361	1440
6.1	(1258)	-----	-----
6.2	(1361)	-----	-----
GR6	(951)	-----	-----
		1441	1520
6.1	(1338)	-----	-----
6.2	(1441)	-----	-----
GR6	(1031)	-----	-----
		1521	1600
6.1	(1418)	-----	-----
6.2	(1521)	-----	-----
GR6	(1111)	-----	-----
		1601	1680
6.1	(1498)	-----	-----
6.2	(1601)	-----	-----
GR6	(1191)	-----	-----
		1681	1760
6.1	(1578)	-----	-----
6.2	(1681)	-----	-----
GR6	(1271)	-----	-----
		1761	1840
6.1	(1658)	-----	-----
6.2	(1761)	-----	-----
GR6	(1351)	-----	-----
		1841	1920
6.1	(1738)	-----	-----
6.2	(1841)	-----	-----
GR6	(1431)	-----	-----
		1921	2000
6.1	(1818)	-----	-----
6.2	(1921)	-----	-----
GR6	(1511)	-----	-----
		2001	2080
6.1	(1898)	-----	-----
6.2	(2001)	-----	-----
GR6	(1591)	-----	-----
		2081	2160
6.1	(1978)	-----	-----
6.2	(2081)	-----	-----
GR6	(1671)	-----	-----
		2161	2240
6.1	(2058)	-----	-----
6.2	(2161)	-----	-----
GR6	(1751)	-----	-----

Figure 1 (cont.)

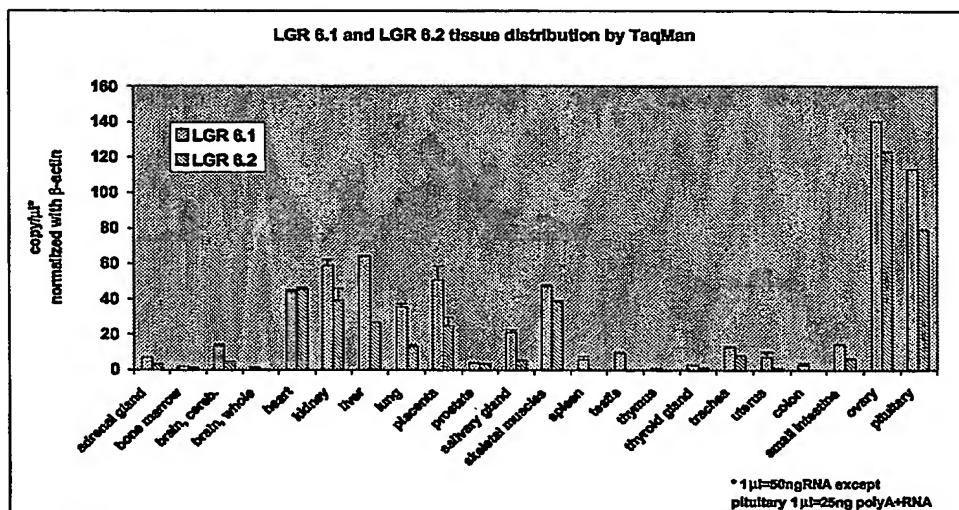
		2241	2320
LGR6.1 (2138)			
LGR6.2 (2241)			
LGR6 (1831)			
		2321	2400
LGR6.1 (2218)			
LGR6.2 (2321)			
LGR6 (1911)			
		2401	2480
6.1 (2298)			
6.2 (2401)			
LGR6 (1991)			
		2481	2560
6.1 (2378)			
6.2 (2481)			
LGR6 (2071)			
		2561	2640
6.1 (2458)			
6.2 (2561)			
LGR6 (2151)			
		2641	2720
6.1 (2538)			
6.2 (2641)			
LGR6 (2231)			
		2721	2800
6.1 (2618)			
6.2 (2721)			
LGR6 (2311)			
		2801	2880
6.1 (2698)			
6.2 (2801)			
LGR6 (2391)			
		2881	2960
6.1 (2778)			
6.2 (2881)			
LGR6 (2471)			
		2961	3040
6.1 (2858)			
6.2 (2961)			
LGR6 (2485)			
		3041	3120
6.1 (2938)			
6.2 (3041)			
LGR6 (2485)			
		3121	3200
6.1 (3018)			
6.2 (3121)			
LGR6 (2485)			
		3201	3280
6.1 (3098)			
6.2 (3201)			
LGR6 (2485)			
		3281	3360
6.1 (3178)			
6.2 (3281)			
LGR6 (2485)			

Figure 1 (cont.)

		3361		3440
LGR6.1	(3258)	GAATTAAGCTTGGAAAGGCTTGC	AAAAAAAAAATAAATAAATAA	
LGR6.2	(3361)	GAATTAAGCTTGGGAGGCTTAA	AAAAAAAAAAAAAAAAAAAAAAAA	
LGR6	(2485)			
		3441	3451	
LGR6.1	(3307)	-----		
LGR6.2	(3441)	AAAAAAAAAA		
LGR6	(2485)	-----		

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Figure 2



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Figure 3

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LGR6      MRLEGEGRSARAGQNLSPAGSARRGAPRDLSMNNLTQLPGLFHHLRFLLEELRLSGNHLS
LGR6.1    ---MGRPRLTLVCQ-VSIIISAR-----DLSMNNLTQLPGLFHHLRFLLEELRLSGNHLS
LGR6.2    ---MGRPRLTLVCQ-VSIIISAR-----DLSMNNLTQLPGLFHHLRFLLEELRLSGNHLS
          * . * : . * : *      ***      *****

LGR6      HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSL -----
LGR6.1    HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
LGR6.2    HIPGQAFSGLYSLKILMLQNNQLGGIPAEALWELPSLQSLRLDANLISLVPERSFEGLS
          *****

:6        -----
:6.1      LRHLWLDNALTEIPVRALNN LPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQ
:6.2      LRHLWLDNALTEIPVRALNNLPALQAMTLALNRISHIPDYAFQNLTSLVVLHLHNNRIQ

:6        -----DLNYNKLQEFFVAIRTLGRLQELGFHNNN IKAIPKAFMGNPLL
:6.1      HLGTHSFEGHNNLETLDLNYNKLQEFFVAIRTLGRLQELGFHNNNIKAIPKAFMGNPLL
:6.2      HLGTHSFEGHNNLETLDLNYNKLQEFFVAIRTLGRLQELGFHNNNIKAIPKAFMGNPLL
          *****

:6        QTIHFYDNPIQFVGRSAFYQLPKLHTLSLNGAMDIQEFFDLKGTTSLEILTLAGIRLL
:6.1      QTIHFYDNPIQFVGRSAFYQLPKLHTLSLNGAMDIQEFFDLKGTTSLEILTLAGIRLL
:6.2      QTIHFYDNPIQFVGRSAFYQLPKLHTLSLNGAMDIQEFFDLKGTTSLEILTLAGIRLL
          *****

:6        PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEI GLQHNRIWEIGADTFSQLSSLOAL
:6.1      PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEI GLQHNRIWEIGADTFSQLSSLOAL
:6.2      PSGMCQQLPRLRVLELSHNQIEELPSLHRCQKLEEMRS -----
          *****

:6        DLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLGKGNLALSQAFSKD
:6.1      DLSWNAIRSIHPEAFSTLHSLVKLDLTDNQLTTLPLAGLGGLMHLKLGKGNLALSQAFSKD
:6.2      -----GGLYLEPPS-----
          *** . * .

:6        SFPKLRILEVP YAYOCCPYGMCASFFKASGQWEADLHLDDEESSKRPLGLLARQAENHY
:6.1      SFPKLRILEVP YAYOCCPYGMCASFFKASGQWEADLHLDDEESSKRPLGLLARQAENHY
:6.2      -----ARGAWSGARV-----
          * * * . . :

:6        DQDLDELQLEMEDSKPHPSVQCSPTP GEFKPCYLFESWGIRLAVWAI VLLSVLCNGLVL
:6.1      DQDLDELQLEMEDSKPHPSVQCSPTP GEFKPCYLFESWGIRLAVWAI VLLSVLCNGLVL
:6.2      -----

:6        LTVFAGGPVPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCR
:6.1      LTVFAGGPVPLPPVKFVVGAIAGANTLTGISCGLLASVDALTFGQFSEYGARWETGLGCR
:6.2      -----

:6        ATGFLAVLGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAAL
:6.1      ATGFLAVLGSEASVLLLTAAVQCSVSVSCVRAYGKSPSLGSVRAGVLGCLALAGLAAAL
:6.2      -----

:6        PLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNSFCFLVVGAYIKLYCDLP
:6.1      PLASVGEYGASPLCLPYAPPEGQPAALGFTVALVMNSFCFLVVGAYIKLYCDLP
:6.2      -----

:6        EAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLN
:6.1      EAVWDCAMVRHVAVLIFADGLLYCPVAFLSFASMLGLFPVTPEAVKSVLLVVLPLPACLN
:6.2      -----

```

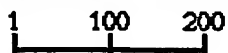
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Figure 3 (cont.)

LGR6	PLLYLLFNPHFRDDLRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEAS
LGR6.1	PLLYLLFNPHFRDDLRLRPRAGDSGPLAYAAAGELEKSSCDSTQALVAFSDVDLILEAS
LGR6.2	-----
LGR6	EAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGS
LGR6.1	EAGRPPGLETYGFPSVTLISCQQPGAPRLEGSHCVEPEGNHFGNPQPSMDGELLRAEGS
LGR6.2	-----
36	TPAGGGLSGGGGFQPSGLALLHTY
36.1	TPAGGGLSGGGGFQPSGLAFASHV
36.2	-----

**Figure 4.**

**Domains within the query sequence LGR6 of 828 residues**



**mainly within the query sequence LGR6.1 of 915 residues**



**mains within the query sequence LGR6.2 of 348 residues**



transmembrane segments as predicted by the *TMHMM2* program (▬), coiled coil regions determined by *Coils2* program (▬) and Segments of low compositional complexity, determined by the *SEG* program (▬), signal peptides determined by the *SignalP* program (▬), GPI anchors are indicated by (▬). Regions containing repeats detected by *Prospero*, but not covered by domains are indicated by (▬).